

M. Ibrahim

ENTERED



OIEP

RAW SEQUENCE LISTING

DATE: 08/05/2003

PATENT APPLICATION: US/09/771,045B

TIME: 10:46:23

Input Set : N:\EBONY'S\US09771045B.raw.txt

Output Set: N:\CRF4\08052003\I771045B.raw

```

1 <110> APPLICANT: Duvick, Johnathan P.
2   Gilliam, Jacob T.
3   Maddox, Joyce R.
4   Rao, Aragula Gururaj
5   Crasta, Oswald R.
6   Folkerts, Otto
7 <120> TITLE OF INVENTION: Amino Polyol Aamine Oxidase Polynucleotides and Related
Polypeptides and
8   Methods of Use
9 <130> FILE REFERENCE: 1134R
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/771,045B
11 <141> CURRENT FILING DATE: 2003-05-16
12 <150> PRIOR APPLICATION NUMBER: US 60/092,936
13 <151> PRIOR FILING DATE: 1998-07-25
14 <150> PRIOR APPLICATION NUMBER: US 60/135,391
15 <151> PRIOR FILING DATE: 1999-05-21
16 <150> PRIOR APPLICATION NUMBER: US 09/352,159
17 <151> PRIOR FILING DATE: 1999-07-12
18 <150> PRIOR APPLICATION NUMBER: US 09/352,168
19 <151> PRIOR FILING DATE: 1999-07-12
20 <160> NUMBER OF SEQ ID NOS: 54
21 <170> SOFTWARE: PatentIn version 3.1
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24 <211> LENGTH: 372
25 <212> TYPE: DNA
26 <213> ORGANISM: Exophiala spinifera
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28 <221> NAME/KEY: misc_feature
29 <222> LOCATION: (346)..(346)
30 <223> OTHER INFORMATION: n = A, T, C, or G
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33   gcttggactg ttgggaccac ttccgtcccg ggtctccgac catgaaacag gtaatggacc   120
34   attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatggggtca cagctcgatt   180
35   ggaggacgcc cgagaagcct tgttcgcgcc accacggctt gtcccatacg aagactatct   240
36   tgctatagta gccagagata gaattttccg ccaatgcttg cttctcggcg ggaagaggtg   300
W--> 37   gtgaaaatgt caaggtggga tacaagggtg tcggtaacga aaccancacc tttttgcttc   360
38   ggaacacggc gc                                     372
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41 <211> LENGTH: 182
42 <212> TYPE: DNA
43 <213> ORGANISM: Exophiala spinifera
44 <400> SEQUENCE: 2
45   gaattttccg ccaatgcttg cttctcggcg ggaagaggtg gtgaaaatgt caaggtggga   60

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46      tacaagggttg tcggtaacga aaccaccacc tttttgcttc ggaacacggc gcccgaggcc 120
47      gatcgtactg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgaggtgc 180
48      ac 182
50 <210> SEQ ID NO: 3
51 <211> LENGTH: 29
52 <212> TYPE: DNA
53 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <223> OTHER INFORMATION: Designed oligonucleotide for 3' RACE N21965 (Exophiala
spinifera)
56 <400> SEQUENCE: 3
57      tggtttcggtt accgacaacc ttgtatccc 29
59 <210> SEQ ID NO: 4
60 <211> LENGTH: 28
61 <212> TYPE: DNA
62 <213> ORGANISM: Artificial Sequence
63 <220> FEATURE:
64 <223> OTHER INFORMATION: Designed oligonucleotide for 5' RACE 21968
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74 <222> LOCATION: (1)..(1386)
75 <223> OTHER INFORMATION:
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79      1 5 10 15
80      gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt 96
81      Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
82      20 25 30
83      gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144
84      Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
85      35 40 45
86      ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192
87      Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
88      50 55 60
89      agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240
90      Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
91      65 70 75 80
92      ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac 288
93      Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
94      85 90 95
95      ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag 336
96      Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
97      100 105 110

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Input Set : N:\EBONY'S\US09771045B.raw.txt

Output Set: N:\CRF4\08052003\I771045B.raw

98	gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc	384
99	Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile	
100	115 120 125	
101	gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg	432
102	Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg	
103	130 135 140	
104	ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg	480
105	Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	
106	145 150 155 160	
107	cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt	528
108	Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
109	165 170 175	
110	gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag	576
111	Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
112	180 185 190	
113	agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg	624
114	Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	
115	195 200 205	
116	cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg	672
117	Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met	
118	210 215 220	
119	tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct	720
120	Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala	
121	225 230 235 240	
122	gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc	768
123	Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly	
124	245 250 255	
125	gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg	816
126	Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu	
127	260 265 270	
128	tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca	864
129	Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala	
130	275 280 285	
131	ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta	912
132	Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val	
133	290 295 300	
134	tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa	960
135	Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln	
136	305 310 315 320	
137	tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc	1008
138	Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val	
139	325 330 335	
140	gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg	1056
141	Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg	
142	340 345 350	
143	aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac	1104
144	Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp	
145	355 360 365	
146	caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg	1152

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147      Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
148          370                      375                      380
149      gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga      1200
150      Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
151          385                      390                      395                      400
152      gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg      1248
153      Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
154          405                      410                      415
155      gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg      1296
156      Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
157          420                      425                      430
158      tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa      1344
159      Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
160          435                      440                      445
161      cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag      1389
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163          450                      455                      460
165 <210> SEQ ID NO: 6
166 <211> LENGTH: 462
167 <212> TYPE: PRT
168 <213> ORGANISM: Exophiala spinifera
169 <400> SEQUENCE: 6
170      Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
171          1                      5                      10                      15
172      Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
173          20                      25                      30
174      Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
175          35                      40                      45
176      Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
177          50                      55                      60
178      Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
179          65                      70                      75                      80
180      Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
181          85                      90                      95
182      Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
183          100                     105                     110
184      Val Ala Ser Ala Leu Ala Glu Leu Pro Val Trp Ser Gln Leu Ile
185          115                     120                     125
186      Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
187          130                     135                     140
188      Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
189          145                     150                     155                     160
190      Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
191          165                     170                     175
192      Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
193          180                     185                     190
194      Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
195          195                     200                     205
196      Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met

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197          210          215          220
198 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
199 225          230          235          240
200 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
201          245          250          255
202 Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu
203          260          265          270
204 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
205          275          280          285
206 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
207          290          295          300
208 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
209 305          310          315          320
210 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
211          325          330          335
212 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
213          340          345          350
214 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
215          355          360          365
216 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
217          370          375          380
218 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
219 385          390          395          400
220 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
221          405          410          415
222 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
223          420          425          430
224 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
225          435          440          445
226 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
227          450          455          460

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229 <210> SEQ ID NO: 7

230 <211> LENGTH: 1442

231 <212> TYPE: DNA

232 <213> ORGANISM: Exophiala spinifera

233 <220> FEATURE:

234 <221> NAME/KEY: CDS

235 <222> LOCATION: (1)..(645)

236 <223> OTHER INFORMATION:

237 <220> FEATURE:

238 <221> NAME/KEY: Intron

239 <222> LOCATION: (646)..(698)

240 <223> OTHER INFORMATION:

W--> 241 <220>

242 <221> NAME/KEY: CDS

243 <222> LOCATION: (699)..(1439)

244 <223> OTHER INFORMATION:

W--> 245 <400> 7

246 gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg

48

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/771,045B

DATE: 08/05/2003
TIME: 10:46:24

Input Set : N:\EBONY'S\US09771045B.raw.txt
Output Set: N:\CRF4\08052003\I771045B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 346
Seq#:39; N Pos. 649
Seq#:40; Xaa Pos. 216

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 7
Seq#:3; Line(s) 55
Seq#:12; Line(s) 639
Seq#:13; Line(s) 649
Seq#:20; Line(s) 1136
Seq#:21; Line(s) 1253
Seq#:26; Line(s) 1904
Seq#:27; Line(s) 2123
Seq#:30; Line(s) 2704
Seq#:31; Line(s) 2965
Seq#:32; Line(s) 3142
Seq#:33; Line(s) 3269

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/771,045B

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Input Set : N:\EBONY'S\US09771045B.raw.txt

Output Set: N:\CRF4\08052003\I771045B.raw

L:10 M:270 C: Current Application Number differs, Wrong Format
L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:300
L:76 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:0
L:241 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:0
L:245 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:0
L:245 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:0
L:477 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:0
L:684 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:0
L:881 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:18,Line#:0
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L:1334 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:22,Line#:0
L:1558 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:24,Line#:0
L:1930 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:26,Line#:0
L:2277 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:28,Line#:0
L:2730 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:30,Line#:0
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L:3628 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:39,Line#:0
L:3632 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:39,Line#:0
L:3643 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:600
L:3702 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:208
L:3765 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:41,Line#:0
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STATISTICS SUMMARY

DATE: 08/05/2003

PATENT APPLICATION: US/09/771,045B

TIME: 10:46:24

Input Set : N:\EBONY'S\US09771045B.raw.txt

Output Set: N:\CRF4\08052003\I771045B.raw

Application Serial Number: US/09/771,045B

Alpha or Numeric or Xml: Numeric

Application Class:

Application File Date: 05-16-2003

Art Unit: OIPE

Software Application: PatentIN3.1

Total Number of Sequences: 54

Total Nucleotides: 42754

Total Amino Acids: 14748

Number of Errors: 0

Number of Warnings: 32

Number of Corrections: 1

MESSAGE SUMMARY

258 W: 29 (Mandatory Feature missing)

270 C: 1 (Current Application Number differs)

341 W: 3 ((46) "n" or "Xaa" used)